

STIC-Biotech/ChemLib

180886

From: Walicka, Malgorzata  
Sent: Tuesday, February 28, 2006 4:42 PM  
To: STIC-Biotech/ChemLib

Please search SEQ ID NO:14, 15, 16 and 17 in case 10/763,249.

Thank you.

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400 Dulany St.  
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Mail Room 2C70  
Tel. (571) 272-0944, fax (571) 273-0944

STIC

02/28/06

02/28/06

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2006, 01:09:25 ; Search time 26.0409 Seconds

(without alignments)  
1245.158 Million cell updates/sec

Title: US-10-763-249-15

Perfect score: 1837  
Sequence: 1.MPNNGSQYHTEGAMQTLTP.....LYRAADQMARLLDPLEEA 337

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*

1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of residues predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1491	81.2	323	2 B83010	prolyl aminopeptid
2	974.5	53.0	313	2 B82671	proline imino-pept
3	970.5	52.8	316	2 AC1965	proline imino-pept
4	957.5	52.1	338	2 AB3453	prolyl aminopeptid
5	925.5	50.4	320	2 B87401	proline imino-pept
6	924.5	50.3	329	2 B84515	proline imino-pept
7	921	50.1	318	2 AD2708	proline imino-pept
8	921	50.1	318	2 B87490	proline imino-pept
9	909	49.5	316	2 AC0217	proline imino-pept
10	901	49.0	317	2 JCS666	prolyl aminopeptid
11	837.5	45.6	310	2 F81878	prolyl aminopeptid
12	836.5	45.5	310	2 G39592	probable prolyl am
13	835.5	45.5	310	2 B81141	prolyl aminopeptid
14	643	35.0	361	2 B81141	proline imino-pept
15	593	32.3	323	2 T35734	proline imino-pept
16	532	29.0	309	2 S73458	probable aminopept
17	467.5	25.4	308	2 B64202	prolyl aminopeptid
18	192	10.5	281	2 S18245	prolyl aminopeptid
19	188.5	10.3	283	2 T31275	xyLF protein - pse
20	184	10.0	286	2 JCS419	2-hydroxymuconate-
21	183.5	10.0	294	2 A59087	prolyl aminopeptid
22	174	9.5	276	2 JH0245	2-hydroxy-6-oxohp
23	173	9.4	330	2 G87401	epoxide hydrolase
24	168.5	9.2	299	2 S68980	leucyl aminopeptid
25	168.5	9.2	310	2 D90495	tricorn protease
26	167	9.1	293	2 T37465	probable prolyl am
27	166.5	9.0	286	2 G70948	hypothetical prote
28	165.5	9.0	266	2 A69358	carboxylesterase (
29	165	9.0	283	2 S10773	2-hydroxymuconic a

30	163	8.9	261	2 T35708	hydrolyase - Strept
31	162.5	8.8	271	2 H97230	alpha/beta superia
32	162	8.8	529	2 T35966	probable secreted
33	161.5	8.8	278	2 S27614	bromide peroxidase
34	161.5	8.8	309	2 D90679	hypothetical prote
35	161.5	8.8	309	2 H85529	hypothetical prote
36	160.5	8.7	309	1 E64762	probable 2,6-dioxo
37	160	8.7	276	2 S76992	probable bromide p
38	160	8.7	221	2 G70605	hypothetical prote
39	158.5	8.6	304	2 E70607	arylester hydrolas
40	154	8.4	302	2 AB3196	probable epib prot
41	153.5	8.4	356	2 F70636	probable bpoc prot
42	150	8.2	262	2 E70548	acetoin dehydrogen
43	150	8.2	283	2 B87546	probable acetyltra
44	149	8.1	266	2 G90785	probable acetyltra
45	149	8.1	266	2 E85645	

#### ALIGNMENTS

RESULT 1	B83010	prolyl aminopeptidase PA5080 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species:	Pseudomonas aeruginosa	
C/Date:	15-Sep-2000	#sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession:	B83010	
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B		
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lim		
.; Lory, S.; Olson, M.V.		
Nature 406, 959-964, 2000		
A/Title:	Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path	
A/Reference number:	A82950; MUID:20437337; PMID:10984043	
A/Accession:	B83010	
A/Status:	Preliminary	
A/Molecule type:	DNA	
A/Residues:	1-323 <STO>	
A/Cross-references:	UNIPROT:Q9HUA3; UNIPARC:UP100000CSEEE; GB:AE004921; GB:AE004091; NI	
A/Experimental source:	strain PA01	
C/Genetics:		
A/Gene:	PA5080	
C/Superfamily:	proline aminopeptidase	
Query Match	81.2% Score 1491; DB 2; Length 323;	
Best Local Similarity	81.9% Pred. No. 8.3e-123;	
Matches	263; Conservative 32; Mismatches 26; Indels 0; Gaps 0;	
QY	15	MOTLYPOIKPYARDLVAEPHVLVYDESSGPEGLPVYFIRGCGAGCDAOSRCYFDNLT 74
DB	1	MLVLYPEIKPYARHDLVDEPHVLVYADSSGPDGLPVYFVGGSGCCDALSRFFDNL 60
QY	75	YRIITFDGRCGRSTPHASLENNNTTWHLVEDLERIREHLDGDKWVLFQSGSGSTLALAYA 134
DB	61	YRIITFDGRCGRSTPHASLENNNTTWHLVEDLERIREHLDGDKWVLFQSGSGSTLALAYA 120
QY	135	QTHERRVHGLIKRIFCRPOEIEWFYQEGASRLFPDYWDYIAPIPPEERGDLVKAFFK 194
DB	121	QTHERRVHGLIKRIFCRPOEIEWFYQEGASRLFPDYWDYIAPIPPEERGDLVKAFFK 180
QY	195	RLTGNDQIAQMAKAKASTWEGRTATLRPNPIVYDRSEFQALSTARIEGHYMANAFL 254
DB	181	RLTGNDQIAQMAKAKASTWEGRTATLRPNPIVYDRSEFQALSTARIEGHYMANAFL 240
QY	255	EPDQILNDLPKIAHLPAVIVHGRYDVICPLDNMAALHQAQNPSELKVIYRDAGHAASEPGI 314
DB	241	RPNQILNDLPKIAHLPAVIVHGRYDVICPLDNMAALHQAQNPSELKVIYRDAGHAASEPGI 300
QY	315	TDALVRAADQMARLLDPLEE 335
DB	301	VDALVRAADQMARLLDPLEE 321

RESULT 2

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 4, 2006, 01:02:32 ; Search time 162.883 Seconds  
(without alignment)  
1459.714 Million cell updates/sec

Title: US-10-763-249-15  
Sequence: 1 MPMNGSQYRTECAMQTLTP.....LVRAADQMARLLDPLEEA 337

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues  
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Uniprot 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1746	95.0	323	2	Q8BD01 PSEPK
2	1601	87.2	323	2	Q4KIM6 PSEPK
3	1543	84.0	323	2	Q4Z2H7 PSEPK
4	1530	83.3	323	2	Q87UX8 PSEPK
5	1491	81.2	323	2	Q9HUA3 PSEPK
6	1454	79.2	321	2	Q4IUN2 AZOVI
7	1006.5	54.8	313	2	Q4UR85 XANCP
8	1006.5	54.8	313	2	Q8PC98 XANCP
9	1003.5	54.6	313	2	Q8ENY0 XANCP
10	1001.5	54.5	315	2	Q7NKP2 GLOVI
11	994	54.1	357	2	Q4LW33 GLOVI
12	990.5	53.9	315	2	Q6MHR0 BDEBA
13	988.5	53.8	313	2	Q5GWM5 XANOR
14	983.5	53.5	313	1	PIP_XYLF
15	983.5	53.5	321	1	PIP_PLEBO
16	979	53.3	312	2	Q62A61 BURMA
17	976	53.1	312	2	Q6JN08 BURPS
18	974.5	53.0	313	1	PIP_XYLF
19	971.5	52.9	313	1	PIP_XANCI
20	970.5	52.8	315	2	Q7WQ23 BOBR
21	970.5	52.8	315	2	Q8IXE3 ANSP
22	965.5	52.6	315	2	Q7WC24 BOBPA
23	957.5	52.1	316	2	Q57F44 BRUAB
24	957.5	52.1	316	2	Q8GK55 BRUSU
25	957.5	52.1	338	2	Q8YF84 BRUCEA
26	956.5	52.1	315	2	Q7V622 BOBPE
27	956	52.0	316	2	Q92R16 RHIME
28	927	50.5	318	2	Q984X4 RHILU
29	925.5	50.4	320	2	Q9A8X1 CAUCR
30	925.5	50.4	322	2	Q5Y297 NOCPA
31	925.5	50.4	380	2	Q93Y05 ARATH

32	924.5	50.3	329	1	PIP_ARATH	P93732 arabidopsis
33	922	50.2	317	2	Q7N3M4 PHOLI	Q7N3M4 photorhabd
34	921	50.1	318	2	Q8UG38 AGRTS	Q8UG38 agrobacteri
35	916.5	49.9	316	2	Q5LWK9 SILPO	Q5LWK9 silibacte
36	916.5	49.9	319	2	Q6ACM6 LEIXX	Q6ACM6 leifsonia x
37	916.5	49.9	329	2	Q94IB5 ARATH	Q94IB5 arabidopsis
38	909	49.5	316	2	Q8ZPD3 YERPE	Q8ZPD3 yersinia pe
39	905	49.3	320	2	Q8XTB7 RALSO	Q8XTB7 ralsonia s
40	905	49.3	341	2	Q5AK21 DICDI	Q5AK21 dictyosteli
41	902	49.1	316	2	Q66BV9 YERPS	Q66BV9 yersinia ps
42	901	49.0	317	1	PIP_SERMA	Q32449 serritella ma
43	887.5	48.3	351	2	Q4PH11 USTMA	Q4PH11 ustiliago ma
44	875.5	47.7	316	2	Q607M2 METCA	Q607M2 methylococ
45	869	47.3	319	2	Q5X473 LEGRA	Q5X473 legionella

## ALIGNMENTS

RESULT 1  
ID Q8BD01 PSEPK PRELIMINARY; PRT; 323 AA.  
AC Q8BD01  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Proline iminopeptidase.  
GN Name=PIP; OrderedLocustNames=PP5028;  
OS Pseudomonas putida (strain KT2440).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=160488;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=22423060; PubMed=12534463;  
RX DOI=10.1046/j.1462-2920.2002.00366.x;  
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,  
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,  
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,  
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,  
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,  
RA Moralez A., Urtreback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,  
RA Wedler H., Lauber J., Stjepandic D., Hohnes J., Straetz M., Helm S.,  
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuenmler B.,  
RA Frazer C.M.,  
RA "Complete genome sequence and comparative analysis of the  
metabolically versatile Pseudomonas putida KT2440.";  
RL Environ. Microbiol. 4:799-808(2002).  
DR EMBL; AB016792; AAN70593.1; -; Genomic\_DNA.  
DR HSP; P52279; IACW.  
DR MEROPS; S33.001; -.  
DR TIGR; PP5028; -.  
DR GO; GO:0005737; C:cytoplasm; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0016804; F:prolyl aminopeptidase activity; IEA.  
DR GO; GO:0014393; F:aromatic compound catabolism; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000073; A/B hydrolase.  
DR InterPro; IPR003089; AB hydrolase.  
DR InterPro; IPR000639; Epox\_hydrolase.  
DR InterPro; IPR005944; Pept\_S33.  
DR InterPro; IPR002410; Peptidase\_S33.  
DR InterPro; IPR000379; Ser\_estr.  
DR Pfam; PF00561; Abhydrolase\_1; 1.  
DR PRINTS; PR00111; ABHYDROLASE.  
DR PRINTS; PR00412; EPOHYDROLASE.  
DR PRINTS; PR00793; PROAMNOPTASE.  
DR TIGRfam; TIGR01249; pro\_imino\_pep\_1; 1.  
KW Complete proteome.  
SQ  
SEQUENCE 323 AA; 36590 MW; 8044637B6A90BAA CRC64;  
Query Match 95.0%; Score 1746; DB 2; Length 323;  
Best Local Similarity 99.4%; Pred. No. 5.8e-139;

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Matches 321; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 15 MÖTLTPOIKPYARHDLAVEAPHVLYVDESGSPGGLPVFTHGGAGAGCDASRCYFPDNL 74
DB 1 MÖTLTPOIKPYARHDLAVEAPHVLYVDESGSPGGLPVFTHGGAGAGCDASRCYFPDNL 60
QY 75 YRITTFDORCGGSRSTPHASLENNNTTWMLVEDLERIREHLGIDKMWLFSGSGSTLALAYA 134
DB 61 YRITTFDORCGGSRSTPHASLENNNTTWMLVEDLERIREHLGIDKMWLFSGSGSTLALAYA 120
QY 135 QTHBERVHGLIRGIFLCRPOEIMFYOGASRLFPDYWDYIAPIPPEERGDIVKAFHK 194
DB 121 QAHBERVHGLIRGIFLCRPOEIMFYOGASRLFPDYWDYIAPIPPEERGDIVKAFHK 180
QY 195 RLITNDIOIAQHAAKAWSTWEGRTATLRPNPLVYDRSEEPORALSIARIECHYPMNNAFL 254
DB 181 RLITNDIOIAQHAAKAWSTWEGRTATLRPNPLVYDRSEEPORALSIARIECHYPMNNAFL 240
QY 255 EPDQILRDLPKIAHLPVAVHGRYDVICPLDNAMALHQAMPNSCLKYTRDAGHAASEPGI 314
DB 241 EPDQILRDLPKIAHLPVAVHGRYDVICPLDNAMALHQAMPNSCLKYTRDAGHAASEPGI 300
QY 315 TDALVRAADQMARRLDLPLEEA 337
DB 301 TDALVRAADQMARRLDLPLEEA 323

RESULT 2
O4KJMB_PSEFS PRELIMINARY; PRT; 323 AA.
ID O4KJMB_PSEFS PRELIMINARY; PRT; 323 AA.
AC O4KJMB_PSEFS PRELIMINARY; PRT; 323 AA.
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DE Proline iminopeptidase (EC 3.4.11.5).
GN Name=Pip; ORFNames=PFL_0411;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=PF-5;
RX PubMed=1598061; DOI=10.1038/nbt110;
RA Paulsen I.T., Press C., Kavel J., Kobayashi D., Myers G.S.,
RA Maurin D., Deboy R.T., Sehadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Macklin K., Tran K.,
RA Kouri H.M., Pierson E., Pierson L., Thomas L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878 (2005).
DR EMBL; CP000076; AAY95820.1; -; Genomic_DNA.
KW Aminopeptidase; Hydrolase.
SQ SEQUENCE 323 AA; 36378 MW; DAFAB82442E008A3 CRC64;

Query Match 87.2%; Score 1601; DB 2; Length 323;
Best Local Similarity 91.3%; Pred. No. 1e-126;
Matches 295; Conservative 9; Mismatches 19; Indels 0; Gaps 0;
QY 15 MÖTLTPOIKPYARHDLAVEAPHVLYVDESGSPGGLPVFTHGGAGAGCDASRCYFPDNL 74
DB 1 MÖTLTPOIKPYARHDLAVEAPHVLYVDESGSPGGLPVFTHGGAGAGCDASRCYFPDNL 60
QY 75 YRITTFDORCGGSRSTPHASLENNNTTWMLVEDLERIREHLGIDKMWLFSGSGSTLALAYA 134
DB 61 YRITTFDORCGGSRSTPHASLENNNTTWMLVEDLERIREHLGIDKMWLFSGSGSTLALAYA 120
QY 135 QTHBERVHGLIRGIFLCRPOEIMFYOGASRLFPDYWDYIAPIPPEERGDIVKAFHK 194
DB 121 QTHBERVHGLIRGIFLCRPOEIMFYOGASRLFPDYWDYIAPIPPEERGDIVKAFHK 180
QY 195 RLITNDIOIAQHAAKAWSTWEGRTATLRPNPLVYDRSEEPORALSIARIECHYPMNNAFL 254
DB 181 RLITNDIOIAQHAAKAWSTWEGRTATLRPNPLVYDRSEEPORALSIARIECHYPMNNAFL 240

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DB 181 RLITNDIOIAQHAAKAWSTWEGRTATLRPNPLVYDRSEEPORALSIARIECHYPMNNAFL 240
QY 255 EPDQILRDLPKIAHLPVAVHGRYDVICPLDNAMALHQAMPNSCLKYTRDAGHAASEPGI 314
DB 241 EPDQILRDLPKIAHLPVAVHGRYDVICPLDNAMALHQAMPNSCLKYTRDAGHAASEPGI 300
QY 315 TDALVRAADQMARRLDLPLEEA 337
DB 301 TDALVRAADQMARRLDLPLEEA 323

RESULT 3
O4Z2H7_PSESY PRELIMINARY; PRT; 323 AA.
ID O4Z2H7_PSESY PRELIMINARY; PRT; 323 AA.
AC O4Z2H7_PSESY PRELIMINARY; PRT; 323 AA.
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DE Peptidase S33, proline iminopeptidase 1 (EC 3.4.11.5).
GN ORFNames=Pyr_0375;
OS Pseudomonas syringae pv. syringae B728a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RG DOE Joint Genome Institute;
RA Chain P., Larimer F., Dibartolo G., Copeland A., Lytkide A., Trong S.,
RA Nolan M., Goldstein E., Thiel J., Malfatti S., Lapidus A., Detter J.C.,
RA Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;
RT "Comparison of two complete genome sequences of Pseudomonas syringae
RT pv. syringae B728a and pv. tomato DC3000."
RT Proc. Natl. Acad. Sci. U.S.A. 0:0-0 (2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Loper J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RX PubMed=1598061; DOI=10.1038/nbt110;
RA Paulsen I.T., Press C., Kavel J., Kobayashi D., Myers G.S.,
RA Maurin D., Deboy R.T., Sehadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Macklin K., Tran K.,
RA Kouri H.M., Pierson E., Pierson L., Thomas L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878 (2005).
DR EMBL; CP000076; AAY95820.1; -; Genomic_DNA.
KW Aminopeptidase; Hydrolase.
SQ SEQUENCE 323 AA; 36435 MW; 3DIBCC11414EF16 CRC64;

Query Match 84.0%; Score 1543; DB 2; Length 323;
Best Local Similarity 86.4%; Pred. No. 8.1e-122;
Matches 279; Conservative 21; Mismatches 23; Indels 0; Gaps 0;
QY 15 MÖTLTPOIKPYARHDLAVEAPHVLYVDESGSPGGLPVFTHGGAGAGCDASRCYFPDNL 74
DB 1 MÖTLTPOIKPYARHDLAVEAPHVLYVDESGSPGGLPVFTHGGAGAGCDASRCYFPDNL 60
QY 75 YRITTFDORCGGSRSTPHASLENNNTTWMLVEDLERIREHLGIDKMWLFSGSGSTLALAYA 134
DB 61 YRITTFDORCGGSRSTPHASLENNNTTWMLVEDLERIREHLGIDKMWLFSGSGSTLALAYA 120

```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 4, 2006, 01:09:25 ; Search time 24.9591 Seconds  
(without alignments)  
1245.158 Million cell updates/sec

Title: US-10-763-249-17

Perfect score: 1753  
Sequence: 1 MQLTYPOIKPYVRHDLAVDE.....LVRAAGDMARRLLDLPPEA 323

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR.80:\*  
2: p1r1:\*  
3: p1r2:\*  
4: p1r3:\*  
5: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1423	81.2	323	2	B83010
2	969.5	55.3	313	2	B82671
3	969.5	55.3	316	2	AC1965
4	938.5	53.5	338	2	AB3453
5	904	51.6	318	2	AD2708
6	904	51.6	318	2	B97490
7	889.5	50.7	320	2	B87401
8	882	50.3	329	2	B84515
9	873	49.8	317	2	JC5696
10	858	48.9	316	2	AC0217
11	830.5	47.4	310	2	S39592
12	823.5	47.0	310	2	F81878
13	821.5	46.9	310	2	B81141
14	625	35.7	361	2	B87435
15	592	33.8	323	2	T35734
16	554	31.6	309	2	S73458
17	483.5	27.6	308	2	B64202
18	199.5	11.4	283	2	T31275
19	196.5	11.2	286	1	JC5419
20	177	10.1	281	2	S18245
21	175	10.0	276	2	JH0245
22	171.5	9.8	283	2	S10773
23	170.5	9.7	294	2	A59087
24	165	9.4	291	2	G70605
25	164.5	9.4	275	2	A71951
26	163	9.3	299	2	S68980
27	162	9.2	266	2	G90785
28	162	9.2	266	2	E85645
29	161.5	9.2	304	2	E70607

#### ALIGNMENTS

30	161.5	9.2	356	2	F70636	probable ephb prot
31	161	9.2	293	2	T37465	probable prolly am
32	159.5	9.1	330	2	G87401	epoxide hydrolase
33	158	9.0	268	2	H69838	chloride peroxidase
34	157.5	9.0	328	2	S27614	bromide peroxidase
35	156	8.9	318	2	H75490	proline iminopeptid
36	152.5	8.7	271	2	B97230	alpha/beta superfa
37	152.5	8.7	275	2	JW0104	azarene carbazole
38	152	8.7	340	2	H98245	lactone-specific e
39	152	8.7	340	2	AD3040	conserved hypothet
40	152	8.7	529	2	T35966	probable secreted
41	151.5	8.6	297	2	T30900	2-hydroxy-6-oxo-6-
42	150.5	8.6	309	2	D90679	hypothetical prote
43	150.5	8.6	309	2	H85529	hypothetical prote
44	150	8.6	266	2	G64842	probable hydrolase
45	149.5	8.5	266	2	A69358	carboxylesterase (

#### RESULT 1

B83010  
prolyl aminopeptidase PA5080 [Imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: B83010  
R:Stover, C.K.; Pham, X.O.; Eryin, A.D.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: B83010  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-323 <STO>  
A:Cross-references: UNIPROT:Q9HUA3; UNIPARC:UPI000000C5EE6; GB:AE004921; GB:AE004091; NID  
A:Experimental source: Strain PA01  
C:Genetics:  
A:Gene: PA5080  
C:Superfamily: proline aminopeptidase

Query Match 81.2% Score 1423; DB 2; Length 323;  
Best Local Similarity 78.2% Pred. No. 1.2e-116;  
Matches 251; Conservative 33; Mismatches 37; Indels 0; Gaps 0;

QY	1	MQLTYPOIKPYVRHDLAVDETHLYVDESGSPQGLPVYFTHGPGAGCDANSRCYFDPNL	60
DB	1	MLVLYPEIKPYARHDLAVDEPHLYADESGSPDGLPVYFVHGPGSGCDALSRFPDPNL	60
QY	61	YRIYTPORGGGRSTPRASLENNTTWDLVADLERIRHGLIEKVLFGSGWGSTLALAYA	120
DB	61	YRIYTPORGGGRSTPRASLENNTTWDLVADLERIRHGLIEKVLFGSGWGSTLALAYA	120
QY	121	QTHEDRYLGLIVGIFLARPODIOFWYQAGASRLFPDIWQYIAPAEERHDMISAYHK	180
DB	121	QTHEDRYLGLIVGIFLARPODIOFWYQAGASRLFPDIWQYIAPAEERHDMISAYHK	180
QY	181	RLTNSDDIAQMAKASTWEGRMGLGCPSPOLIERSEPORALSIARIECHYFTNNSFL	240
DB	181	RLTNSDDIAQMAKASTWEGRMGLGCPSPOLIERSEPORALSIARIECHYFTNNSFL	240
QY	241	EPNGLIDRMKIALPGIIVHGRYDMICPLDNAMELHQAQWNSSELQVIREAGHAASEBGI	300
DB	241	EPNGLIDRMKIALPGIIVHGRYDMICPLDNAMELHQAQWNSSELQVIREAGHAASEBGI	300
QY	301	TDALVRAAGDMARRLLDLPPE 321	
DB	301	VDALVRAATNBIGRLLDLPPE 321	

RESULT 2